



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

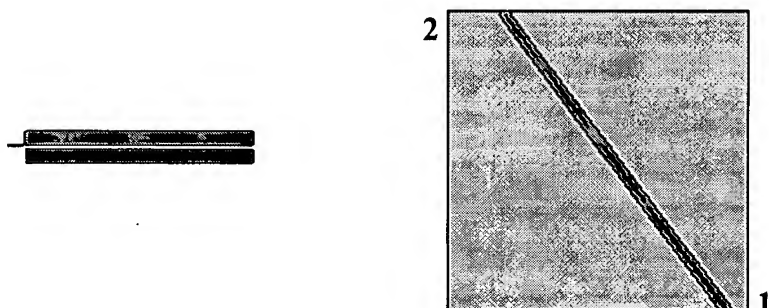
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: [gi|13157532|Human DNA sequence from clone RP11-428G23 on chromosome 13](#)
Contains part of a novel gene (KIAA0916), complete sequence
 Length = 401 (66400 .. 66800)

Sequence 2: [lcl|65536](#)
 Length = 303 (1 .. 303)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 583 bits (303), Expect = 2e-163
 Identities = 303/303 (100%), Gaps = 0/303 (0%)
 Strand=Plus/Minus

Query	66474	CTACCAACCTGTACAGCATGCTGGTGTACTGAATACTGTAGGCAACTGTAACCCATTAGT	66533
Sbjct	303	CTACCAACCTGTACAGCATGCTGGTGTACTGAATACTGTAGGCAACTGTAACCCATTAGT	244
Query	66534	AAGTATTTCTGCATGTAAACATAGAAAAGTTATAGTCAAAGTACTTATTATAATCTTATG	66593
Sbjct	243	AAGTATTTCTGCATGTAAACATAGAAAAGTTATAGTCAAAGTACTTATTATAATCTTATG	184
Query	66594	GGAACACCTTAGCATACGCAGTCCATCACTGACCAAATACTGTTATACAGTGCATAACT	66653

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|||||
Sbjct  183  GGAACACCTTAGCATACGCAGTCCATCACTGACCAAATACTGTTATACAGTGCATAACT 124
Query  66654 GTGTATACACATACATACATATATAGGTATATATATATAAAATAGTGTGTCTGCATGCTT 66713
|||||
Sbjct  123  GTGTATACACATACATACATATATAGGTATATATATATAAAATAGTGTGTCTGCATGCTT 64
Query  66714 ATATATCTTCACAAGAAGAAACACAAGAAGAATAAACTGTAAAACAATGACATTCATTAC 66773
|||||
Sbjct  63   ATATATCTTCACAAGAAGAAACACAAGAAGAATAAACTGTAAAACAATGACATTCATTAC 4
Query  66774 CTC  66776
||||
Sbjct  3     CTC  1
```

CPU time: 0.10 user secs. 0.04 sys. secs 0.14 total secs.